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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,422

DATE: 09/10/2001

TIME: 09:20:17

Input Set : A:\98385Hseq.txt

Output Set: N:\CRF3\09102001\I899422.raw

3 <110> APPLICANT: Hauptmann, Rudolph  
4 Himmeler, Adolph  
5 Maurer-Fogy, Ingrid  
6 Stratowa, Christian  
8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
9 Them  
11 <130> FILE REFERENCE: 98,385-H  
13 <140> CURRENT APPLICATION NUMBER: 09/899,422  
C--> 14 <141> CURRENT FILING DATE: 2001-08-21  
16 <150> PRIOR APPLICATION NUMBER: 09/525,998  
17 <151> PRIOR FILING DATE: 2000-03-15  
19 <150> PRIOR APPLICATION NUMBER: 08/383,676  
20 <151> PRIOR FILING DATE: 1995-02-01  
22 <150> PRIOR APPLICATION NUMBER: 08/153,287  
23 <151> PRIOR FILING DATE: 1993-11-17  
25 <150> PRIOR APPLICATION NUMBER: 07/821,750  
26 <151> PRIOR FILING DATE: 1992-01-02  
28 <150> PRIOR APPLICATION NUMBER: 07/511,430  
29 <151> PRIOR FILING DATE: 1990-04-20  
31 <160> NUMBER OF SEQ ID NOS: 87  
33 <170> SOFTWARE: PatentIn Ver. 2.0  
35 <210> SEQ ID NO: 1  
36 <211> LENGTH: 1368  
37 <212> TYPE: DNA  
38 <213> ORGANISM: Homo sapiens  
40 <220> FEATURE:  
41 <221> NAME/KEY: CDS  
42 <222> LOCATION: (1)..(1368)  
44 <220> FEATURE:  
45 <221> NAME/KEY: sig\_peptide  
46 <222> LOCATION: (1)..(87)  
48 <220> FEATURE:  
49 <221> NAME/KEY: misc\_feature  
50 <222> LOCATION: (88)..(120)  
51 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by  
52 extracellular proteases following secretion.  
54 <220> FEATURE:  
55 <221> NAME/KEY: misc\_feature  
56 <222> LOCATION: (606)..(633)  
57 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by  
58 extracellular proteases following secretion.  
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62 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
63 1 5 10 15  
65 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96  
66 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro

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p. 5

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67	20	25	30	
69	cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa	144		
70	His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys			
71	35 40 45			
73	tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa	192		
74	Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys			
75	50 55 60			
77	gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac	240		
78	Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp			
79	65 70 75 80			
81	tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc	288		
82	Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu			
83	85 90 95			
85	aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg	336		
86	Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val			
87	100 105 110			
89	gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg	384		
90	Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg			
91	115 120 125			
93	aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc	432		
94	Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe			
95	130 135 140			
97	aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag	480		
98	Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu			
99	145 150 155 160			
101	aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa	528		
102	Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu			
103	165 170 175			
105	aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg	576		
106	Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr			
107	180 185 190			
109	aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca	624		
110	Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser			
111	195 200 205			
113	ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt	672		
114	Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu			
115	210 215 220			
117	tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag	720		
118	Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys			
119	225 230 235 240			
121	tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag	768		
122	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
123	245 250 255			
125	ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc	816		
126	Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
127	260 265 270			
129	ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg	864		
130	Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
131	275 280 285			

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133 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt 912
134 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
135      290      295      300
137 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg 960
138 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
139 305      310      315      320
141 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac 1008
142 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
143      325      330      335
145 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac 1056
146 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
147      340      345      350
149 act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg 1104
150 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
151      355      360      365
153 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag 1152
154 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
155      370      375      380
157 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa 1200
158 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
159 385      390      395      400
161 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc 1248
162 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
163      405      410      415
165 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc 1296
166 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
167      420      425      430
169 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc ctc ccg 1344
170 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
171      435      440      445
173 ccc gcg ccc agt ctt ctc aga tga 1368
174 Pro Ala Pro Ser Leu Leu Arg
175      450      455
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 455
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
183 <400> SEQUENCE: 2
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185      1      5      10      15
187 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
188      20      25      30
190 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
191      35      40      45
193 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
194      50      55      60
196 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
197      65      70      75      80
199 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu

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200          85          90          95
202 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
203          100          105          110
205 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
206          115          120          125
208 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
209          130          135          140
211 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
212 145          150          155          160
214 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
215          165          170          175
217 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
218          180          185          190
220 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
221          195          200          205
223 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
224          210          215          220
226 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
227 225          230          235          240
229 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
230          245          250          255
232 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
233          260          265          270
235 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
236          275          280          285
238 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
239          290          295          300
241 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
242 305          310          315          320
244 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
245          325          330          335
247 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
248          340          345          350
250 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
251          355          360          365
253 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
254          370          375          380
256 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
257 385          390          395          400
259 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
260          405          410          415
262 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
263          420          425          430
265 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
266          435          440          445
268 Pro Ala Pro Ser Leu Leu Arg
269          450          455
272 <210> SEQ ID NO: 3
273 <211> LENGTH: 483

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274 <212> TYPE: DNA
275 <213> ORGANISM: Homo sapiens
277 <220> FEATURE:
278 <221> NAME/KEY: CDS
279 <222> LOCATION: (1)..(483)
281 <400> SEQUENCE: 3
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283 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
284 1 5 10 15
286 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt 96
287 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
288 20 25 30
290 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144
291 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
292 35 40 45
294 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 192
295 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
296 50 55 60
298 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 240
299 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
300 65 70 75 80
302 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 288
303 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
304 85 90 95
306 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg 336
307 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
308 100 105 110
310 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc 384
311 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
312 115 120 125
314 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432
315 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
316 130 135 140
318 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480
319 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
320 145 150 155 160
322 aat 483
323 Asn
326 <210> SEQ ID NO: 4
327 <211> LENGTH: 161
328 <212> TYPE: PRT
329 <213> ORGANISM: Homo sapiens
331 <400> SEQUENCE: 4
332 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
333 1 5 10 15
335 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
336 20 25 30
338 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
339 35 40 45

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## VERIFICATION SUMMARY

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Input Set : A:\98385Hseq.txt

Output Set: N:\CRF3\09102001\I899422.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:815 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:1551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:1667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:1670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:1725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36